

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/528,872
Source: PCT/10
Date Processed by STIC: 4/6/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 04/05/2005

PATENT APPLICATION: US/10/528,872

TIME: 12:11:19

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\04052005\J528872.raw

3 <110> APPLICANT: DSM IP ASSETS B.V.
 5 <120> TITLE OF INVENTION: SQS gene
 7 <130> FILE REFERENCE: NDR5218
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/528,872
 C--> 9 <141> CURRENT FILING DATE: 2005-03-23
 9 <150> PRIOR APPLICATION NUMBER: PCT/EP03/10573
 10 <151> PRIOR FILING DATE: 2003-09-23
 12 <150> PRIOR APPLICATION NUMBER: EP 02021619.8
 13 <151> PRIOR FILING DATE: 2002-09-27
 15 <160> NUMBER OF SEQ ID NOS: 8
 17 <170> SOFTWARE: PatentIn version 3.2
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 4807
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Phaffia rhodozyma
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 59 <222> LOCATION: (2398)..(2474)
 61 <220> FEATURE:

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118 atttcctttt ctttctaccc ggagagtaag acacacaaag aatcacgaag aatatgatga      540
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126 gtcgagattc ttttttcttc ttttggtcga gaaaaaaaaa cggcttcgct tcgcacgcgc      780
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130 tcataggtga aggttaaaac ggaatggata ggaggagcta accacgtttt tattttaatt      900
132 cgacttgggc agcctcgtec atagtgtctg atggttatat cgatcataga aggcagcgcc      960
134 tggcgggttc gtcatggccg tgatcatctg ctttgttaga cattgtccat cagtcacctc     1020
136 aatgacagtt tcccagcgcc atcactaaga cacaaacgta tccagcacgc catgtccatc     1080
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140 cttgatcaga cccgacttat gaatatggcc gttattgtac acttcttggt gtcctcgag 1200
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152 ctttcttccg tcttctcttc tctctcttcg tctgaacatc agcatcatc atg ggc ata 1558
153                                     Met Gly Ile
154                                     1
156 tca gat tac ctc gtt ctg g gtcagttctg tcttttggtt gattcttata 1607
157 Ser Asp Tyr Leu Val Leu
158 5
160 ttcttgccgg cggtcgcctg tcttgggtat atcatcagca atgagaaaca tgatgttccc 1667
162 cccgcgtcaa tcaactgacct ttgtgtctc tacttctttc ctgtcgaatt gatcctgatt 1727
164 gatacgtgtg ccggtgctt aacag ct ttc acg cat cct gtaggtgtt 1776
165                                     Ala Phe Thr His Pro
166                                     10
168 tatcgtatgc ttcattgtga tgtttagtca cgcggactga cctggccgggt tgattttctg 1836
170 tatgatcgct tgtgtctaccg tctttcttgg aaatccttcc catcag gcc gat ctg 1891
171                                     Ala Asp Leu
172                                     15
174 cga gct tta atg cag tac gcg atc tgg cat gag cct cga agg aat atc 1939
175 Arg Ala Leu Met Gln Tyr Ala Ile Trp His Glu Pro Arg Arg Asn Ile
176 20 25 30
178 act gca cag gag gaa cat gca aca tcc ggt tgg gac cga gaa act atg 1987
179 Thr Ala Gln Glu Glu His Ala Thr Ser Gly Trp Asp Arg Glu Thr Met
180 35 40 45
182 aag gaa tgt tgg aag tat ttg gat ctg act tca aga agt ttc gca gct 2035
183 Lys Glu Cys Trp Lys Tyr Leu Asp Leu Thr Ser Arg Ser Phe Ala Ala
184 50 55 60 65
186 gtc atc aaa gag ttg gac gga gat ctt acc cga gtc gtacgtgtt 2081
187 Val Ile Lys Glu Leu Asp Gly Asp Leu Thr Arg Val
188 70 75
190 tcattcttctc tctcctttga gatctggctg cctccgcatt ttcttggtgc agaaggggtca 2141
192 gaagctgaca acaccatctc tactgttcgg gacacggcta g atc tgt tta ttc tat 2197
193                                     Ile Cys Leu Phe Tyr
194                                     80
196 ctc gct ctt cga gga ctg gat acc att gag gat gac atg agt cta tct 2245
197 Leu Ala Leu Arg Gly Leu Asp Thr Ile Glu Asp Asp Met Ser Leu Ser
198 85 90 95
200 aat gat gtg aag ctt ccc ctg ctt cgg aca ttc tgg gaa aag ctt gac 2293
201 Asn Asp Val Lys Leu Pro Leu Leu Arg Thr Phe Trp Glu Lys Leu Asp
202 100 105 110
204 tcc cct ggg tgg acc ttt act gga tcc ggt cca aat gag aag gat aga 2341
205 Ser Pro Gly Trp Thr Phe Thr Gly Ser Gly Pro Asn Glu Lys Asp Arg
206 115 120 125 130
208 gag ctt ctt gtt cac ttc gat gtg gcc atc gcc gag ttt gcc aac ttg 2389
209 Glu Leu Leu Val His Phe Asp Val Ala Ile Ala Glu Phe Ala Asn Leu
210 135 140 145

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212 gac gtc aa gtgagtttcc ctttatgggtt ggatcatccg ctcgacagac 2437
213 Asp Val Asn
216 tcgaaacgct catcactttg gtctgcttga tgaacag c tct cgg aac gtc att 2490
217 Ser Arg Asn Val Ile
218 150
220 cga gac atc act cgc aag atg ggt aac ggt atg gcc gac ttt gct tct 2538
221 Arg Asp Ile Thr Arg Lys Met Gly Asn Gly Met Ala Asp Phe Ala Ser
222 155 160 165 170
224 ctc tct acg ccc tcc aag cct gtg gcc gag gtc cag tcg acc gaa gat 2586
225 Leu Ser Thr Pro Ser Lys Pro Val Ala Glu Val Gln Ser Thr Glu Asp
226 175 180 185
228 ttc aac cta tac tgt cat tac gtc gct gga ctc gtc ggc gag gga ctc 2634
229 Phe Asn Leu Tyr Cys His Tyr Val Ala Gly Leu Val Gly Glu Gly Leu
230 190 195 200
232 tcc cga ctc ttt gtc gcg acc gag aag gaa cga cca ttc ttg gcc aac 2682
233 Ser Arg Leu Phe Val Ala Thr Glu Lys Glu Arg Pro Phe Leu Ala Asn
234 205 210 215
236 cag atg gta ctt tca aac tcg ttc gga ctc ctt ctc caa aag aca aac 2730
237 Gln Met Val Leu Ser Asn Ser Phe Gly Leu Leu Leu Gln Lys Thr Asn
238 220 225 230
240 atc ctt cga gat att cgg gag gac gcc gac gaa ggt cgt ggc ttc tgg 2778
241 Ile Leu Arg Asp Ile Arg Glu Asp Ala Asp Glu Gly Arg Gly Phe Trp
242 235 240 245 250
244 cca aga gag atc tgg gcc aac ccg atc tat act gcg cat gca ccg ggc 2826
245 Pro Arg Glu Ile Trp Ala Asn Pro Ile Tyr Thr Ala His Ala Pro Gly
246 255 260 265
248 aca agg ttt aac tcg ttg act gac ctg gtc aag aaa gaa aac atc gac 2874
249 Thr Arg Phe Asn Ser Leu Thr Asp Leu Val Lys Lys Glu Asn Ile Asp
250 270 275 280
252 aaa gga tca atg tgg gtg ttg agt gcg atg aca ctc gac gcg atc acc 2922
253 Lys Gly Ser Met Trp Val Leu Ser Ala Met Thr Leu Asp Ala Ile Thr
254 285 290 295
256 cat act acc gac gca ctg gac tac ctc tca ctt cta aag aac cag agt 2970
257 His Thr Thr Asp Ala Leu Asp Tyr Leu Ser Leu Leu Lys Asn Gln Ser
258 300 305 310
260 gtt ttc aac ttt tgt gct atc ccg gct gtc atg tcg att gca acg ttg 3018
261 Val Phe Asn Phe Cys Ala Ile Pro Ala Val Met Ser Ile Ala Thr Leu
262 315 320 325 330
264 gag cta tgc ttc atg aac cca gcg gtg ttc caa cga aac ata aaa atc 3066
265 Glu Leu Cys Phe Met Asn Pro Ala Val Phe Gln Arg Asn Ile Lys Ile
266 335 340 345
268 aga aag gga gaa gcc gtc gag gtgcgttcgc gcgttctgtt tctacctttc 3117
269 Arg Lys Gly Glu Ala Val Glu
270 350
272 ataacattgg aggttcttga ctcttaagcg tcttccaatc tgatgcctcc aattatcatc 3177
274 atttttgtct tttttgcttt cctcttgttt cttttcggcg tgattcaatc cag ctc 3233
275 Leu
278 att atg aag tgc aac aac cct cgg gag gtg gca tac atg ttt aga gat 3281
279 Ile Met Lys Cys Asn Asn Pro Arg Glu Val Ala Tyr Met Phe Arg Asp

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284          375          380          385
286 atc aag ttg agc gtt gcg tgt ggt cga gtgagttgat cgatcgatcc      3376
287 Ile Lys Leu Ser Val Ala Cys Gly Arg
288          390          395
290 atctttttgtt ttgatcatcg cgagacttga ctgatcgatt actcaaaaca tcatcgcttc      3436
292 tccttcttgc tctctag atc gaa caa tgg gct gag cac t gtatgttcct      3485
293          Ile Glu Gln Trp Ala Glu His
294          400
296 ccgccccctcc ttcaagtttc ctctcgcttc atctttgttg agaagaggga tctgatgtat      3545
298 ctttctttgt tcggatcag ac tac ccc tca ttt atg atg att cgg cct tcg      3596
299          Tyr Tyr Pro Ser Phe Met Met Ile Arg Pro Ser
300          405          410
302 aat gac cct caa aac ccc gca ccc tca acg gcg ctt gac cct ttc tca      3644
303 Asn Asp Pro Gln Asn Pro Ala Pro Ser Thr Ala Leu Asp Pro Phe Ser
304          415          420          425
306 gga gac gct cgt tta agg ata gcc tct aag aag gct gag atc acc gcc      3692
307 Gly Asp Ala Arg Leu Arg Ile Ala Ser Lys Lys Ala Glu Ile Thr Ala
308 430          435          440          445
310 gct gct ctt gtc agg aag aaa gcc cgg gat cac gct aag tgg aga gag      3740
311 Ala Ala Leu Val Arg Lys Lys Ala Arg Asp His Ala Lys Trp Arg Glu
312          450          455          460
314 tcc aag gga ttg cct ccg agc gat ccg aac aag ccg gac aac tcg gag      3788
315 Ser Lys Gly Leu Pro Pro Ser Asp Pro Asn Lys Pro Asp Asn Ser Glu
316          465          470          475
318 gat gtt aat tgg gta ttg atc ggc ggt atg atc gtt gga ttg ttg ctc      3836
319 Asp Val Asn Trp Val Leu Ile Gly Gly Met Ile Val Gly Leu Leu Leu
320          480          485          490
322 gtg atg ggc gtg ctc ggt ttg gct atc gct tgg gtt gtt ctt cag      3881
323 Val Met Gly Val Leu Gly Leu Ala Ile Ala Trp Val Val Leu Gln
324          495          500          505
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328 cttactctgt catacag ttt gag caa taa tctcaagatt ctagtccatc      3990
329          Phe Glu Gln
330          510
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348 gacacttgac cgattcgtta ataaagccgt cccacctttt tctttaatgg caattcaaga      4530
350 agagaaaaaac aaccctgcg cgcaactcgag tagtcgatca gaccttccga acgacagata      4590
352 tcatttgctg aaatcgaccg gattttaaag ctgctgccag gtcggtgaat cccctagggt      4650
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 3,6,12,15
Seq#:5; N Pos. 3,9,15,18,21
Seq#:6; N Pos. 3,6,9,12,15

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5,6,7,8

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0

L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0

L:747 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0